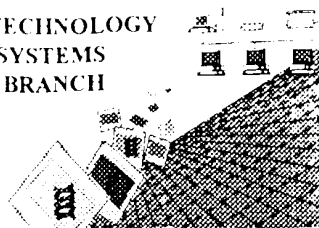


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/050,216
Source: OIPR
Date Processed by STIC: 2/6/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/050,716

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) 7 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002
TIME: 19:11:09

ppr 1-5

Input Set : A:\SEQUENCE LISTING.txt
Output Set : N:\CRF3\02062002\J050216.raw

Does Not Comply
Corrected File Name

4 <110> APPLICANT: Curtis, Rory A.J., Lora, Jose M.
6 <120> TITLE OF INVENTION: 46798, A HUMAN MATRIX METALLOPROTEINASE
7 AND USES THEREFOR
9 <130> FILE REFERENCE: MPI2001-014P1RCPl(M)
OK 11 <140> CURRENT APPLICATION NUMBER: US/10/050,216
OK 11 <141> CURRENT FILING DATE: 2002-01-16
11 <160> NUMBER OF SEQ ID NOS: 10
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

224 <210> SEQ ID NO: 3
225 <211> LENGTH: 1335
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (1)...(1335)
233 <400> SEQUENCE: 3

ppr 1-3

E-->	234	atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg cag ctg cta ctg	48
	235	Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu	
	236	1 5 10 15	
E-->	238	tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg	96
	239	Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu	
	240	20 25 30	
E-->	242	cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa	144
	243	Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu	
	244	35 40 45	
E-->	246	cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga	
	247	Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg	
	248	50 55 60	
E-->	250	gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc	
	251	Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg	
	252	65 70 75 80	
E-->	254	gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc	
	255	Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr	
	256	85 90 95	
E-->	258	aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga	
	259	Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg	
	260	100 105 110	
E-->	262	cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc	
	263	His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly	

*Suggestion:
Consult
Sequence Rules
for valid format*

*48 insert
cumulative
base totals
at right
margin of
each line*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002

TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\02062002\J050216.raw

```

      264          115          120          125
E--> 266 gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac
      267 Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
      268          130          135          140
E--> 270 caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc
      271 Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
      272 145          150          155          160
E--> 274 gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tgc
      275 Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
      276          165          170          175
E--> 278 ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag agg ctg ggc cgc
      279 Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
      280          180          185          190
E--> 282 gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat
      283 Asp Ala Leu Leu Ser Trp Asp Val Leu Ala Val Gln Ser Leu Tyr
      284          195          200          205
E--> 286 ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg
      287 Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
      288          210          215          220
E--> 290 ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc
      291 Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
      292 225          230          235          240
E--> 294 cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc
      295 Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
      296          245          250          255
E--> 298 act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc
      299 Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
      300          260          265          270
E--> 302 tgg gag gtg gca gct gat ggc aac gtc tca gag ccc cgt cca ctg cag
      303 Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
      304          275          280          285
E--> 306 gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca
      307 Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
      308          290          295          300
E--> 310 ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg
      311 Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg
      312 305          310          315          320
E--> 314 ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca
      315 Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
      316          325          330          335
E--> 318 ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc ttc cct cct ctg
      319 Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
      320          340          345          350
E--> 322 cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga
      323 Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
      324          355          360          365
E--> 326 ggg gga ctg caa gtg gag ccc tac tac ccc cga agt ctg cag gac tgg
      327 Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
      328          370          375          380

```

insert
Cumulative
base totals

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002

TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\02062002\J050216.raw

E--> 330 gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc
 331 Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
 332 385 390 395 400
 E--> 334 tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc
 335 Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
 336 405 410 415
 E--> 338 aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg
 339 Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
 340 420 425 430
 E--> 342 atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc
 343 Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
 344 435 440 445
 391 <210> SEQ ID NO: 6
 392 <211> LENGTH: 471
 393 <212> TYPE: PRT
 394 <213> ORGANISM: Homo sapiens
 396 <400> SEQUENCE: 6
 397 Met His Pro Gly Val Leu Ala Ala Phe Leu Phe Leu Ser Trp Thr His
 398 1 5 10 15
 399 Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser
 400 20 25 30
 401 Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
 402 35 40 45
 403 Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
 404 50 55 60
 405 Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
 406 65 70 75 80
 407 Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
 408 85 90 95
 409 Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
 410 100 105 110
 411 Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
 412 115 120 125
 413 Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
 414 130 135 140
 415 Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
 416 145 150 155 160
 417 Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr
 418 165 170 175
 419 Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly
 420 180 185 190
 421 Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
 422 195 200 205
 423 Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
 424 210 215 220
 425 Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
 426 225 230 235 240
 427 Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
 428 245 250 255

insert
total

see
4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002

TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\02062002\J050216.raw

429 Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
 430 260 265 270
 431 Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
 432 275 280 285
 433 Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
 434 290 295 300
 435 Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
 436 305 310 315 320
 437 Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
 438 325 330 335
 439 Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
 440 340 345 350
 441 Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
 442 355 360 365
 443 Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
 444 370 375 380
 445 Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
 446 385 390 395 400
 447 Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
 448 405 410 415
 449 Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
 450 420 425 430
 451 Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
 452 435 440 445
 453 Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
 454 450 455 460
 455 Ala Asn Ser Ile Leu Trp Cys
 456 465 470
 458 <211> LENGTH: 56
 459 <212> TYPE: PRT
 460 <213> ORGANISM: Homo sapiens
 462 <223> OTHER INFORMATION: The X at positions 2-5 can be any amino acid.
 464 <223> OTHER INFORMATION: The amino acid at position 7 can be as few as 21,
 465 up to 25, amino acids, and the amino acid can be
 466 any amino acid.
 468 <223> OTHER INFORMATION: The X at positions 9-12 can be any amino acid.
 470 <223> OTHER INFORMATION: The X at position 16 can be any amino acid.
 472 <223> OTHER INFORMATION: The X at position 18 can be any amino acid.
 474 <223> OTHER INFORMATION: The X at positions 21-22 can be any amino acid.
 476 <223> OTHER INFORMATION: The X at positions 25-26 can be any amino acid.
 478 <223> OTHER INFORMATION: The X at positions 27-28 can be any amino acid.
 480 <223> OTHER INFORMATION: The amino acid at position 37 can be as few as 26,
 481 up to 71, amino acids, and the amino acid can be
 482 any amino acid.
 484 <223> OTHER INFORMATION: The X at position 39 can be any amino acid.
 486 <223> OTHER INFORMATION: The X at position 42 can be any amino acid.
 488 <223> OTHER INFORMATION: The X at position 48 can be any amino acid.
 490 <223> OTHER INFORMATION: The amino acid at position 50 can be as few as 4,
 491 up to 87 amino acids, and the amino acid can be

initial-
 see
 item 5
 on Error

Summary
 Sheet

see
 item 5

item 5

see p. 5

<2107> insert this mandatory residue identifier and response
 <220> insert this whenever <2217, <2227, or
 <2237 is present

28-29
 what about Xaa at position 35?

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002
TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\02062002\J050216.raw

492 any amino acid.

494 <223> OTHER INFORMATION: The X at position 52 can be any amino acid.

496

E--> 496 <400> SEQUENCE: 7

W--> 497 Leu Xaa Xaa Xaa Xaa Tyr Xaa Gln Xaa Xaa Xaa Xaa Leu Pro Val Xaa

498 1 5 10 15

W--> 499 Gly Xaa Leu Asp Xaa Xaa Thr Leu Xaa Xaa Met Xaa Xaa Pro Arg Cys

500 20 25 30

W--> 501 Gly Val Xaa Asp Xaa Phe Xaa Gly Gly Xaa Leu Ala His Ala Phe Xaa

502 35 40 45

W--> 503 Pro Xaa Gly Xaa Ala His Phe Asp

E--> 504 50

E--> 508 <210> SEQ ID NO: 8

*SS ← number the amino acids under every 5
amino acids.*

*DO NOT use TAB
codes between
the numbers;
use space characters*

VERIFICATION SUMMARY

DATE: 02/06/2002

PATENT APPLICATION: US/10/050,216

TIME: 19:11:10

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\02062002\J050216.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:234 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:3
M:254 Repeated in SeqNo=3
L:496 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:496 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:7
L:497 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:497 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:497 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:499 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:499 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:499 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:501 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:501 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:501 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:503 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:503 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:503 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:504 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:504 M:252 E: No. of Seq. differs, <211>LENGTH:Input:7 Found:56 SEQ:0
L:508 M:214 E: (33) Seq.# missing, SEQ ID NO:7